**Figure S2.** The sequences of motif 1 to motif 10 of BES1 gene family among examined species.
Figure S3. The conversed motifs (M1 to M10) analyses for each group using the MEME program.
Figure S4. The sequences alignment of F1, F2, and F3 subgroups among examined species. The Glyco_hydro_14 domain contained in F1 and F2 subgroups is marked using the blue dashed box in F3 subgroup.
Figure S5. The analyses of Glyco_hydro_14 domain, including (a) protein structure, (b) alignment with the homology model (1fa2.1.A), (c) prediction of local similarity to target, (d) comparison with non-redundant set of PDB structures.
Figure S6. The analyses of orthologous BES1 genes between *O. sativa* and other examined species. (a) The interaction network constructed using the orthologous gene pairs between *O. sativa* and other species. (b) The number of orthologous genes in each species with 6 *O. sativa* BES1 genes.
Figure S7. The analyses of orthologous $BES1$ genes between $A.\ trichopoda$ and other examined species. (a) The interaction network constructed using the orthologous gene pairs between $A.\ trichopoda$ and other species. (b) The number of orthologous genes in each species with 4 $A.\ trichopoda\ BES1$ genes.
Figure S8. The analyses of orthologous BES1 genes between *S. moellendorffii* and other examined species. (a) The interaction network constructed using the orthologous gene pairs between *S. moellendorffii* and other species. (b) The number of orthologous genes in each species with 4 *S. moellendorffii* BES1 genes.
Figure S9. The analyses of orthologous BES1 genes between *P. patens* and other examined species. (a) The interaction network constructed using the orthologous gene pairs between *P. patens* and other species. (b) The number of orthologous genes in each species with 6 *P. patens* BES1 genes.
Figure S10. The analyses of paralogous BESI genes in each of the examined species. The green lines indicated the 4 *B. napus* BESI genes, which had more than 1 paralogous genes.
Figure S11. The reconstructed phylogenetic tree according to the duplication and losses of BES1 genes at different stages of plant evolution.
Figure S12. The histogram of BES1 genes expression in root and leaf of B. napus. The genes marked with green located subgenome A, and red located subgenome C of B. napus.